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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: Thu Oct 18 15:52:58 EDT 2007

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Application No: 10784528 Version No: 2.0

**Input Set:**

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**Finished:** 2007-10-02 19:27:39.130  
**Elapsed:** 0 hr(s) 0 min(s) 0 sec(s) 713 ms  
**Total Warnings:** 2  
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**No. of SeqIDs Defined:** 10  
**Actual SeqID Count:** 10

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
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## SEQUENCE LISTING

<110> BROWN, ARTHUR M.  
WIBLE, BARBARA A.

<120> METHODS OF INDUCING APOPTOSIS IN HYPERPROLIFERATION  
CELLS

<130> 22884/04085

<140> 10784528  
<141> 2004-02-23

<150> 10/000,778

<151> 2001-10-31

<160> 10

<170> PatentIn Ver. 3.3

<210> 1  
<211> 1725  
<212> DNA  
<213> Homo sapiens

<220>

<221> CDS  
<222> (1)..(1722)

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ggg ccc tct gat ctc tcc ctt ctc tct ttg ccc cct ggc acc tct cct 96  
Gly Pro Ser Asp Leu Ser Leu Ser Leu Pro Pro Gly Thr Ser Pro  
20 25 30

gta ggc tcc cct ggt cct cta gct ccc att ccc cca acg ctg ttg gcc 144  
Val Gly Ser Pro Gly Pro Leu Ala Pro Ile Pro Pro Thr Leu Leu Ala  
35 40 45

cct ggc acc ctg ctg ggc ccc aag cgt gag gtg gac atg cac ccc cct 192  
Pro Gly Thr Leu Leu Gly Pro Lys Arg Glu Val Asp Met His Pro Pro  
50 55 60

ctg ccc cag cct gtg cac cct gat gtc acc atg aaa cca ttg ccc ttc 240  
Leu Pro Gln Pro Val His Pro Asp Val Thr Met Lys Pro Leu Pro Phe  
65 70 75 80

tat gaa gtc tat ggg gag ctc atc cgg ccc acc acc ctt gca tcc act 288  
Tyr Glu Val Tyr Gly Glu Leu Ile Arg Pro Thr Thr Leu Ala Ser Thr  
85 90 95

tct agc cag cgg ttt gag gaa gcg cac ttt acc ttt gcc ctc aca ccc 336  
Ser Ser Gln Arg Phe Glu Ala His Phe Thr Phe Ala Leu Thr Pro

100	105	110	
cag caa gtg cag cag att ctt aca tcc aga gag gtt ctg cca gga gcc Gln Gln Val Gln Gln Ile Leu Thr Ser Arg Glu Val Leu Pro Gly Ala			384
115	120	125	
aaa tgt gat tat acc ata cag gtg cag cta agg ttc tgt ctc tgt gag Lys Cys Asp Tyr Thr Ile Gln Val Gln Leu Arg Phe Cys Leu Cys Glu			432
130	135	140	
acc agc tgc ccc cag gaa gat tat ttt ccc ccc aac ctc ttt gtc aag Thr Ser Cys Pro Gln Glu Asp Tyr Phe Pro Pro Asn Leu Phe Val Lys			480
145	150	155	160
gtt aat ggg aaa ctg tgc ccc ctg ccg ggt tac ctt ccc cca acc aag Val Asn Gly Lys Leu Cys Pro Leu Pro Gly Tyr Leu Pro Pro Thr Lys			528
165	170	175	
aat ggg gcc gag ccc aag agg ccc agc cgc ccc atc aac atc aca ccc Asn Gly Ala Glu Pro Lys Arg Pro Ser Arg Pro Ile Asn Ile Thr Pro			576
180	185	190	
ctg gct cga ctc tca gcc act gtt ccc aac acc att gtg gtc aat tgg Leu Ala Arg Leu Ser Ala Thr Val Pro Asn Thr Ile Val Val Asn Trp			624
195	200	205	
tca tct gag ttc gga cgg aat tac tcc ttg tct gtg tac ctg gtg agg Ser Ser Glu Phe Gly Arg Asn Tyr Ser Leu Ser Val Tyr Leu Val Arg			672
210	215	220	
cag ttg act gca gga acc ctt cta caa aaa ctc aga gca aag ggt atc Gln Leu Thr Ala Gly Thr Leu Leu Gln Lys Leu Arg Ala Lys Gly Ile			720
225	230	235	240
cgg aac cca gac cac tcg cgg gca ctg atc aag gag aaa ttg act gct Arg Asn Pro Asp His Ser Arg Ala Leu Ile Lys Glu Lys Leu Thr Ala			768
245	250	255	
gac cct gac agt gag gtg gcc act aca agt ctc cgg gtg tca ctc atg Asp Pro Asp Ser Glu Val Ala Thr Thr Ser Leu Arg Val Ser Leu Met			816
260	265	270	
tgc ccg cta ggg aag atg cgc ctg act gtc cct tgt cgt gcc ctc acc Cys Pro Leu Gly Lys Met Arg Leu Thr Val Pro Cys Arg Ala Leu Thr			864
275	280	285	
tgt gcc cac ctg cag agc ttc gat gct gcc ctt tat cta cag atg aat Cys Ala His Leu Gln Ser Phe Asp Ala Ala Leu Tyr Leu Gln Met Asn			912
290	295	300	
gag aag aag cct aca tgg aca tgt cct gtg tgt gac aag aag gct ccc Glu Lys Lys Pro Thr Trp Thr Cys Pro Val Cys Asp Lys Lys Ala Pro			960
305	310	315	320
tat gaa tct ctt atc att gat ggt tta ttt atg gag att ctt agt tcc Tyr Glu Ser Leu Ile Ile Asp Gly Leu Phe Met Glu Ile Leu Ser Ser			1008
325	330	335	

tgt tca gat tgt gat gag atc caa ttc atg gaa gat gga tcc tgg tgc			1056
Cys Ser Asp Cys Asp Glu Ile Gln Phe Met Glu Asp Gly Ser Trp Cys			
340	345	350	
cca atg aaa ccc aag aag gag gca tct gag gtt tgc ccc ccg cca ggg			1104
Pro Met Lys Pro Lys Lys Glu Ala Ser Glu Val Cys Pro Pro Pro Gly			
355	360	365	
tat ggg ctg gat ggc ctc cag tac agc cca gtc cag ggg gga gat cca			1152
Tyr Gly Leu Asp Gly Leu Gln Tyr Ser Pro Val Gln Gly Gly Asp Pro			
370	375	380	
tca gag aat aag aag aag gtc gaa gtt att gac ttg aca ata gaa agc			1200
Ser Glu Asn Lys Lys Val Glu Val Ile Asp Leu Thr Ile Glu Ser			
385	390	395	400
tca tca gat gag gag gat ctg ccc cct acc aag aag cac tgt tct gtc			1248
Ser Ser Asp Glu Glu Asp Leu Pro Pro Thr Lys Lys His Cys Ser Val			
405	410	415	
acc tca gct gcc atc ccg gcc cta cct gga agc aaa gga gtc ctg aca			1296
Thr Ser Ala Ala Ile Pro Ala Leu Pro Gly Ser Lys Gly Val Leu Thr			
420	425	430	
tct ggc cac cag cca tcc tcg gtg cta agg agc cct gct atg ggc acg			1344
Ser Gly His Gln Pro Ser Ser Val Leu Arg Ser Pro Ala Met Gly Thr			
435	440	445	
ttg ggt ggg gat ttc ctg tcc agt ctc cca cta cat gag tac cca cct			1392
Leu Gly Gly Asp Phe Leu Ser Ser Leu Pro Leu His Glu Tyr Pro Pro			
450	455	460	
gcc ttc cca ctg gga gcc gac atc caa ggt tta gat tta ttt tca ttt			1440
Ala Phe Pro Leu Gly Ala Asp Ile Gln Gly Leu Asp Leu Phe Ser Phe			
465	470	475	480
ctt cag aca gag agt cag cac tat ggc ccc tct gtc atc acc tca cta			1488
Leu Gln Thr Glu Ser Gln His Tyr Gly Pro Ser Val Ile Thr Ser Leu			
485	490	495	
gat gaa cag gat gcc ctt ggc cac ttc ttc cag tac cga ggg acc cct			1536
Asp Glu Gln Asp Ala Leu Gly His Phe Phe Gln Tyr Arg Gly Thr Pro			
500	505	510	
tct cac ttt ctg ggc cca ctg gcc ccc acg ctg ggg agc tcc cac tgc			1584
Ser His Phe Leu Gly Pro Leu Ala Pro Thr Leu Gly Ser Ser His Cys			
515	520	525	
agc gcc act ccg gcg ccc cct cct ggc cgt gtc agc agc att gtg gcc			1632
Ser Ala Thr Pro Ala Pro Pro Gly Arg Val Ser Ser Ile Val Ala			
530	535	540	
cct ggg ggg gcc ttg agg gag ggg cat gga gga ccc ctg ccc tca ggt			1680
Pro Gly Gly Ala Leu Arg Glu Gly His Gly Gly Pro Leu Pro Ser Gly			
545	550	555	560

ccc tct ttg act ggc tgt cggt cga gac atc att tcc ctg gac tga            1725  
Pro Ser Leu Thr Gly Cys Arg Ser Asp Ile Ile Ser Leu Asp  
              565                                    570

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<211> 574  
<212> PRT  
<213> Homo sapiens

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Gly Pro Ser Asp Leu Ser Leu Leu Ser Leu Pro Pro Gly Thr Ser Pro  
    20    25    30  
  
Val Gly Ser Pro Gly Pro Leu Ala Pro Ile Pro Pro Thr Leu Leu Ala  
    35    40    45  
  
Pro Gly Thr Leu Leu Gly Pro Lys Arg Glu Val Asp Met His Pro Pro  
    50    55    60  
  
Leu Pro Gln Pro Val His Pro Asp Val Thr Met Lys Pro Leu Pro Phe  
65    70    75    80  
  
Tyr Glu Val Tyr Gly Glu Leu Ile Arg Pro Thr Thr Leu Ala Ser Thr  
    85    90    95  
  
Ser Ser Gln Arg Phe Glu Glu Ala His Phe Thr Phe Ala Leu Thr Pro  
    100    105    110  
  
Gln Gln Val Gln Gln Ile Leu Thr Ser Arg Glu Val Leu Pro Gly Ala  
    115    120    125  
  
Lys Cys Asp Tyr Thr Ile Gln Val Gln Leu Arg Phe Cys Leu Cys Glu  
    130    135    140  
  
Thr Ser Cys Pro Gln Glu Asp Tyr Phe Pro Pro Asn Leu Phe Val Lys  
145    150    155    160  
  
Val Asn Gly Lys Leu Cys Pro Leu Pro Gly Tyr Leu Pro Pro Thr Lys  
    165    170    175  
  
Asn Gly Ala Glu Pro Lys Arg Pro Ser Arg Pro Ile Asn Ile Thr Pro  
    180    185    190  
  
Leu Ala Arg Leu Ser Ala Thr Val Pro Asn Thr Ile Val Val Asn Trp  
    195    200    205  
  
Ser Ser Glu Phe Gly Arg Asn Tyr Ser Leu Ser Val Tyr Leu Val Arg  
    210    215    220  
  
Gln Leu Thr Ala Gly Thr Leu Leu Gln Lys Leu Arg Ala Lys Gly Ile  
225    230    235    240  
  
Arg Asn Pro Asp His Ser Arg Ala Leu Ile Lys Glu Lys Leu Thr Ala

245                    250                    255  
Asp Pro Asp Ser Glu Val Ala Thr Thr Ser Leu Arg Val Ser Leu Met  
260                    265                    270  
  
Cys Pro Leu Gly Lys Met Arg Leu Thr Val Pro Cys Arg Ala Leu Thr  
275                    280                    285  
  
Cys Ala His Leu Gln Ser Phe Asp Ala Ala Leu Tyr Leu Gln Met Asn  
290                    295                    300  
  
Glu Lys Lys Pro Thr Trp Thr Cys Pro Val Cys Asp Lys Lys Ala Pro  
305                    310                    315                    320  
  
Tyr Glu Ser Leu Ile Ile Asp Gly Leu Phe Met Glu Ile Leu Ser Ser  
325                    330                    335  
  
Cys Ser Asp Cys Asp Glu Ile Gln Phe Met Glu Asp Gly Ser Trp Cys  
340                    345                    350  
  
Pro Met Lys Pro Lys Lys Glu Ala Ser Glu Val Cys Pro Pro Pro Gly  
355                    360                    365  
  
Tyr Gly Leu Asp Gly Leu Gln Tyr Ser Pro Val Gln Gly Gly Asp Pro  
370                    375                    380  
  
Ser Glu Asn Lys Lys Lys Val Glu Val Ile Asp Leu Thr Ile Glu Ser  
385                    390                    395                    400  
  
Ser Ser Asp Glu Glu Asp Leu Pro Pro Thr Lys Lys His Cys Ser Val  
405                    410                    415  
  
Thr Ser Ala Ala Ile Pro Ala Leu Pro Gly Ser Lys Gly Val Leu Thr  
420                    425                    430  
  
Ser Gly His Gln Pro Ser Ser Val Leu Arg Ser Pro Ala Met Gly Thr  
435                    440                    445  
  
Leu Gly Gly Asp Phe Leu Ser Ser Leu Pro Leu His Glu Tyr Pro Pro  
450                    455                    460  
  
Ala Phe Pro Leu Gly Ala Asp Ile Gln Gly Leu Asp Leu Phe Ser Phe  
465                    470                    475                    480  
  
Leu Gln Thr Glu Ser Gln His Tyr Gly Pro Ser Val Ile Thr Ser Leu  
485                    490                    495  
  
Asp Glu Gln Asp Ala Leu Gly His Phe Phe Gln Tyr Arg Gly Thr Pro  
500                    505                    510  
  
Ser His Phe Leu Gly Pro Leu Ala Pro Thr Leu Gly Ser Ser His Cys  
515                    520                    525  
  
Ser Ala Thr Pro Ala Pro Pro Pro Gly Arg Val Ser Ser Ile Val Ala  
530                    535                    540  
  
Pro Gly Gly Ala Leu Arg Glu Gly His Gly Gly Pro Leu Pro Ser Gly

545

550

555

560

Pro Ser Leu Thr Gly Cys Arg Ser Asp Ile Ile Ser Leu Asp  
565 570

<210> 3

<211> 28

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
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Thr Leu Leu Gly Pro Lys Arg Glu Val Asp Met His

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<210> 4

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
peptide

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<210> 5

<211> 650

<212> PRT

<213> Homo sapiens

<400> 5

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1 5 10 15

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20 25 30

Arg Lys His Glu Leu Leu Thr Lys Ala Leu His Leu Leu Lys Ala Gly  
35 40 45

Cys Ser Pro Ala Val Gln Met Lys Ile Lys Glu Leu Tyr Arg Arg Arg  
50 55 60

Phe Pro Gln Lys Ile Met Thr Pro Ala Asp Leu Ser Ile Pro Asn Val

65

70

75

80

His Ser Ser Pro Met Pro Ala Thr Leu Ser Pro Ser Thr Ile Pro Gln

85

90

95

Leu Thr Tyr Asp Gly His Pro Ala Ser Ser Pro Leu Leu Pro Val Ser

100

105

110

Leu Leu Gly Pro Lys His Lys Leu Glu Leu Pro His Leu Thr Ser Ala

115

120

125

Leu His Pro Val His Pro Asp Ile Lys Leu Gln Lys Leu Pro Phe Tyr

130

135

140

Asp Leu Leu Asp Glu Leu Ile Lys Pro Thr Ser Leu Ala Ser Asp Asn

145

150

155

160

Ser Gln Arg Phe Arg Glu Thr Cys Phe Ala Phe Ala Leu Thr Pro Gln

165

170

175

Gln Val Gln Gln Ile Ser Ser Ser Met Asp Ile Ser Gly Thr Lys Cys

180

185

190

Asp Phe Thr Val Gln Val Gln Leu Arg Phe Cys Leu Ser Glu Thr Ser

195

200

205

Cys Pro Gln Glu Asp His Phe Pro Pro Asn Leu Cys Val Lys Val Asn

210

215

220

Thr Lys Pro Cys Ser Leu Pro Gly Tyr Leu Pro Pro Thr Lys Asn Gly

225

230

235

240

Val Glu Pro Lys Arg Pro Ser Arg Pro Ile Asn Ile Thr Ser Leu Val

245

250

255

Arg Leu Ser Thr Thr Val Pro Asn Thr Met Cys Ser Trp Thr Ala Glu

260

265

270

Ile Gly Arg Asn Tyr Ser Met Ala Val Tyr Leu Val Lys Gln Leu Ser

275

280

285

Ser Thr Val Leu Leu Gln Arg Leu Arg Ala Lys Gly Ile Arg Asn Pro

290

295

300

Asp His Ser Arg Ala Leu Ile Lys Glu Lys Leu Thr Ala Asp Pro Asp

305

310

315

320

Ser Glu Ile Ala Thr Thr Ser Leu Arg Val Ser Leu Leu Cys Pro Leu

325

330

335

Gly Lys Met Arg Leu Thr Ile Pro Cys Arg Ala Leu Thr Cys Ser His

340

345

350

Leu Gln Cys Phe Asp Ala Thr Leu Tyr Ile Gln Met Asn Glu Lys Lys

355

360

365

Pro Thr Trp Val Cys Pro Val Cys Asp Lys Lys Ala Pro Tyr Glu His

370

375

380

Leu Ile Ile Asp Gly Leu Phe Met Glu Ile Leu Lys Tyr Cys Thr Asp  
385 390 395 400

Cys Asp Glu Ile Gln Phe Lys Glu Asp Gly Thr Trp Ala Pro Met Arg  
405 410 415

Ser Lys Lys Glu Val Gln Glu Val Ser Ala Ser Tyr Asn Gly Val Asp  
420 425 430

Gly Cys Leu Ser Ser Thr Leu Glu His Gln Val Ala Ser His His Gln  
435 440 445

Ser Ser Asn Lys Asn Lys Val Glu Val Ile Asp Leu Thr Ile Asp  
450 455 460

Ser Ser Ser Asp Glu Glu Glu Glu Pro Ser Ala Lys Arg Thr Cys  
465 470 475 480

Pro Ser Leu Ser Pro Thr Ser Pro Leu Asn Asn Lys Gly Ile Leu Ser  
485 490 495

Leu Pro His Gln Ala Ser Pro Val Ser Arg Thr Pro Ser Leu Pro Ala  
500